
Sequence Listing was accepted with existing errors.

See attached Validation Report.

If you need help call the Patent Electronic Business Center at (866)

217-9197 (toll free).

Reviewer: Anne Corrigan

Timestamp: Mon Jun 04 19:49:29 EDT 2007

Validated By CRFValidator v 1.0.2

Application No: 10581551 Version No: 1.1

Input Set:

Output Set:

Started: 2007-06-04 19:49:18.416

Finished: 2007-06-04 19:49:22.284

Elapsed: 0 hr(s) 0 min(s) 3 sec(s) 868 ms

Total Warnings: 26

Total Errors: 1

No. of SeqIDs Defined: 84

Actual SeqID Count: 84

Err	or code	Error Description
E	257	Invalid sequence data feature in <221> in SEQ ID (29)
W	213	Artificial or Unknown found in <213> in SEQ ID (59)
W	213	Artificial or Unknown found in <213> in SEQ ID (60)
M	213	Artificial or Unknown found in <213> in SEQ ID (61)
M	213	Artificial or Unknown found in <213> in SEQ ID (62)
W	213	Artificial or Unknown found in <213> in SEQ ID (63)
W	213	Artificial or Unknown found in <213> in SEQ ID (64)
W	213	Artificial or Unknown found in <213> in SEQ ID (65)
W	213	Artificial or Unknown found in <213> in SEQ ID (66)
W	213	Artificial or Unknown found in <213> in SEQ ID (67)
W	213	Artificial or Unknown found in <213> in SEQ ID (68)
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W	213	Artificial or Unknown found in <213> in SEQ ID (73)
\overline{W}	213	Artificial or Unknown found in <213> in SEQ ID (74)
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W	213	Artificial or Unknown found in <213> in SEQ ID (76)
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Input Set:

Output Set:

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Total Warnings: 26

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No. of SeqIDs Defined: 84

Actual SeqID Count: 84

Error code Error Description

W 213 Artificial or Unknown found in <213> in SEQ ID (78)

This error has occured more than 20 times, will not be displayed

SEQUENCE LISTING

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Arg Pi	ro Tyr 35		Gly	His	Gln	Glu 40	Met	Thr	Leu	Arg	Val 45	Thr	Met	Ala
_	ly Gly 50	Pro	Met	Pro	Phe 55	Ala	Phe	Asp	Leu	Val 60	Ser	His	Val	Phe
Cys Ty	yr Gly	His	Arg	Pro 70	Phe	Thr	Lys	Tyr	Pro 75	Glu	Glu	Ile	Pro	Asp
Tyr Ph	ne Lys	Gln	Ala 85	Phe	Pro	Glu	Gly	Leu 90	Ser	Trp	Glu	Arg	Ser 95	Leu
Glu Ph	ne Glu		Gly					Val				Ile 110		Leu

Arg Gly Asn Thr Phe Tyr His Lys Ser Lys Phe Thr Gly Val Asn Phe

125

120

130	-	135	-	140	
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Thr Met Tyr Leu	Lys Leu (Glu Gly Gl	y Gly Asn E 170	His Lys Cys	Gln Phe 175
Lys Thr Thr Tyr	_	Ala Lys Ly 18		Lys Met Pro 190	_
His Tyr Ile Ser 195	His Arg I	Leu Val Ar 200	g Lys Thr (Glu Gly Asn 205	Ile Thr
Glu Leu Val Glu 210	_	Val Ala Hi 215	s Ser		
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Tyr Phe Lys Gln Ala Phe Pro Glu Gly Leu Ser Trp Glu Arg Ser Leu

90

95

85

Pro Ala Asp Gly Pro Ile Met Gln Asn Gln Ser Val Asp Trp Glu Pro

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aag act a Lys Thr T			_		_							_	576
cat tac a His Tyr I 1	_	_		_				_					624
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Arg Pro T	Tyr Glu 35	Gly His	Gln	Glu 40	Met	Thr	Leu	Arg	Val 45	Thr	Met	Ala	
Lys Gly G 50	Gly Pro	Met Pro	Phe 55	Ala	Phe	Asp	Leu	Val 60	Ser	His	Val	Phe	
Cys Tyr G 65	Gly His	Arg Cys		Thr	Lys	Tyr	Pro 75	Glu	Glu	Ile	Pro	Asp 80	
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	ttc Phe	_	_						_					_		336
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	gcc Ala 130	_				_					_					432
	acc Thr															480
	ttg Leu															528
	act Thr			_		_		_								576
	tac Tyr				_		_									624
	ctg Leu 210	_	_	_	_	_	_			taa						657
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Arg	Pro	Tyr 35	Glu	Gly	His	Gln	Glu 40	Met	Thr	Leu	Arg	Val 45	Thr	Met	Ala	
Lys	Gly 50	Gly	Pro	Met	Pro	Phe 55	Ala	Phe	Asp	Leu	Val 60	Ser	His	Val	Phe	

Gly Tyr Gly His Arg Gly Phe Thr Lys Tyr Pro Glu Glu Ile Pro Asp

 65
 70
 75
 80

Tyr Phe Lys Gln Ala Phe Pro Glu Gly Leu Ser Trp Glu Arg Ser Leu
85 90 95

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Pro Ala Asp Gly Pro Ile Met Gln Asn Gln Ser Val Asp Trp Glu Pro 130 135 140

Ser Thr Glu Lys Ile Thr Ala Ser Asp Gly Val Leu Lys Gly Asp Asp 145 150 150

Thr Met Tyr Leu Lys Leu Glu Gly Gly Asn His Lys Cys Gln Met
165 170 175

Lys Thr Thr Tyr Lys Ala Ala Lys Lys Ile Leu Lys Met Pro Gly Ser 180 185 190

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20 25 30

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35 40 45

aag ggc ggg cca atg cct ttc gcg ttt gac tta gtg tca cac gtg ttc 192 Lys Gly Gly Pro Met Pro Phe Ala Phe Asp Leu Val Ser His Val Phe
50 55 60

				_	ggt Gly 70									240
					ttt Phe									288
					ggg									336
_					tac Tyr							_		384
					atc Ile									432
					act Thr 150									480
					ctt Leu									528
					gcg Ala	_		_			_		 _	576
			_		cgc Arg		_			Ī				624
	_	_	_	_	gca Ala	Ō			taa					657

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<213> Fungia sp.

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Arg Pro Tyr Glu Gly His Gln Glu Met Thr Leu Arg Val Thr Met Ala 35

Lys Gly (Gly Pro	Met P	o Phe 55		Phe	Asp	Leu	Val 60	Ser	His	Val	Phe	
Ala Tyr (Gly His	_	y Phe	Thr	Lys	Tyr	Pro 75	Glu	Glu	Ile	Pro	Asp 80	
Tyr Phe	Lys Gln	Ala Pl 85	ne Pro	Glu	Gly	Leu 90	Ser	Trp	Glu	Arg	Ser 95	Leu	
Glu Phe	Glu Asp 100	_	y Ser	Ala	Ser 105	Val	Ser	Ala	His	Ile 110	Ser	Leu	
Arg Gly	Asn Thr 115	Phe T	r His	Lys 120	Ser	Lys	Phe	Thr	Gly 125	Val	Asn	Phe	
Pro Ala . 130	Asp Gly	Pro I	e Met 135		Asn	Gln	Ser	Val 140	Asp	Trp	Glu	Pro	
Ser Thr	Glu Lys		nr Ala 50	Ser	Asp	Gly	Val 155	Leu	Lys	Gly	Asp	Val 160	
Thr Met	Tyr Leu	Lys L	eu Glu	Gly	Gly	Gly 170	Asn	His	Lys	Cys	Gln 175	Phe	
Lys Thr	Thr Tyr 180	_	a Ala	Lys	Lys 185	Ile	Leu	Lys	Met	Pro 190	Gly	Ser	
His Tyr	Ile Ser 195	His A	rg Leu	Val 200	Arg	Lys	Thr	Glu	Gly 205	Asn	Ile	Thr	
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ggc tcc Gly Ser		Gly H					_						96
aga cct Arg Pro													144

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Ser	Thr	Glu	Lys	Ile	Thr	Ala	Ser	Asp	Gly	Val	Leu	ras	Gly	Asp	Val	
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